

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/658,677DATE: 03/27/2003
TIME: 15:31:03

INPUT SET: S36987.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Sheppard, Paul O.

(ii) TITLE OF INVENTION: SERINE PROTEASE POLYPEPTIDES
AND MATERIALS AND METHODS FOR MAKING THEM

(iii) NUMBER OF SEQUENCES: 18

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: ZymoGenetics, Inc.

(B) STREET: 1201 Eastlake Avenue East

(C) CITY: Seattle

(D) STATE: WA

(E) COUNTRY: USA

(F) ZIP: 98102

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette

(B) COMPUTER: IBM Compatible

(C) OPERATING SYSTEM: DOS

(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US/09/658,677

(B) FILING DATE:

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/072,384

(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Parker, Gary E

(B) REGISTRATION NUMBER: 31,648

(C) REFERENCE/DOCKET NUMBER: 97-16C1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 206-442-6673

(B) TELEFAX: 206-442-6678

(C) TELEX:

ENTERED

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47
48 (2) INFORMATION FOR SEQ ID NO:1:
49
50 (i) SEQUENCE CHARACTERISTICS:
51 (A) LENGTH: 1634 base pairs
52 (B) TYPE: nucleic acid
53 (C) STRANDEDNESS: double
54 (D) TOPOLOGY: linear
55
56 (ix) FEATURE:
57
58 (A) NAME/KEY: Coding Sequence
59 (B) LOCATION: 105...1280
60 (D) OTHER INFORMATION:
61
62 (A) NAME/KEY: Signal Sequence
63 (B) LOCATION: 105...161
64 (D) OTHER INFORMATION:
65
66 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
67
68 GGCACGAGGG GGAGCCGCGC GCTCTCTCCC GCGCCCCACA CCTGTCTGAG CGGCGCAGCG 60
69 AGCCGCGGCC CGGGCGGGCT GCTCGGCGCG GAACAGTGCT CGGC ATG GCA GGG ATT 116
70 Met Ala Gly Ile
71
72
73 CCA GGG CTC CTC TTC CTT CTC TTC TTT CTG CTC TGT GCT GTT GGG CAA 164
74 Pro Gly Leu Leu Phe Leu Leu Phe Phe Leu Leu Cys Ala Val Gly Gln
75 -15 -10 -5 1
76
77 GTG AGC CCT TAC AGT GCC CCC TGG AAA CCC ACT TGG CCT GCA TAC CGC 212
78 Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro Thr Trp Pro Ala Tyr Arg
79 5 10 15
80
81 CTC CCT GTC GTC TTG CCC CAG TCT ACC CTC AAT TTA GCC AAG CCA GAC 260
82 Leu Pro Val Val Leu Pro Gln Ser Thr Leu Asn Leu Ala Lys Pro Asp
83 20 25 30
84
85 TTT GGA GCC GAA GCC AAA TTA GAA GTA TCT TCT TCA TGT GGA CCC CAG 308
86 Phe Gly Ala Glu Ala Lys Leu Glu Val Ser Ser Ser Cys Gly Pro Gln
87 35 40 45
88
89
90
91
92 TGT CAT AAG GGA ACT CCA CTG CCC ACT TAC AAA GAA GCC AAG CAA TAT 356
93 Cys His Lys Gly Thr Pro Leu Pro Thr Tyr Lys Glu Ala Lys Gln Tyr
94 50 55 60 65
95
96 CTG TCT TAT GAA ACG CTC TAT GCC AAT GGC AGC CGC ACA GAG ACN CAG 404
97 Leu Ser Tyr Glu Thr Leu Tyr Ala Asn Gly Ser Arg Thr Glu Xaa Gln
98 70 75 80
99

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100	GTG GGC ATC TAC ATC CTC AGC AGT AGT GGA GAT GGG GCC CAN CNC CGA	452
101	Val Gly Ile Tyr Ile Leu Ser Ser Ser Gly Asp Gly Ala Xaa Xaa Arg	
102	85 90 95	
103		
104	GAC TCA GGG TCT TCA GGA AAG TCT CGA AGG AAG CGG CAG ATT TAT GGC	500
105	Asp Ser Gly Ser Ser Gly Lys Ser Arg Arg Lys Arg Gln Ile Tyr Gly	
106	100 105 110	
107		
108	TAT GAC AGC AGG TTC AGC ATT TTT GGG AAG GAC TTC CTG CTC AAC TAC	548
109	Tyr Asp Ser Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr	
110	115 120 125	
111		
112	CCT TTC TCA ACA TCA GTG AAG TTA TCC ACG GGC TGC ACC GGC ACC CTG	596
113	Pro Phe Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu	
114	130 135 140 145	
115		
116	GTG GCA GAA AAN CAT GTC CTC ACA GCT GCC CAC TGC ATA CAC GAT GGA	644
117	Val Ala Glu Xaa His Val Leu Thr Ala Ala His Cys Ile His Asp Gly	
118	150 155 160	
119		
120	AAA ACC TAT GTG AAA GGA ACC CAG AAG CTT CGA GTC GGC TTC CTA AAG	692
121	Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu Lys	
122	165 170 175	
123		
124	CCC AAG TTT AAA GAT GGT GGT CGA GGG GCC AAC GAC TCC ACT TCA GCC	740
125	Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr Ser Ala	
126	180 185 190	
127		
128	ATG CCC GAG CAG ATG AAA TTT CAG TGG ATC CGG GTG AAA CGC ACC CAT	788
129	Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys Arg Thr His	
130	195 200 205	
131		
132	GTG CCC AAG GGT TGG ATC AAG GGC AAT GCC AAT GAC ATC GGC ATG GAT	836
133	Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp Ile Gly Met Asp	
134	210 215 220 225	
135		
136		
137		
138	TAT GAT TAT GCC CTC CTG GAA CTC AAA AAG CCC CAC AAG AGA AAA TTT	884
139	Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro His Lys Arg Lys Phe	
140	230 235 240	
141		
142	ATG AAG ATT GGG GTG AGC CCT CCT GCT AAG CAG CTG CCA GGG GGC AGA	932
143	Met Lys Ile Gly Val Ser Pro Pro Ala Lys Gln Leu Pro Gly Gly Arg	
144	245 250 255	
145		
146	ATT CAC TTC TCT GGT TAT GAC AAT GAC CGA CCA GGC AAT TTG GTG TAT	980
147	Ile His Phe Ser Gly Tyr Asp Asn Asp Arg Pro Gly Asn Leu Val Tyr	
148	260 265 270	
149		
150	CGC TTC TGT GAC GTC AAA GAC GAG ACC TAT GAC TTG TTG TAC CAG CAA	1028
151	Arg Phe Cys Asp Val Lys Asp Glu Thr Tyr Asp Leu Leu Tyr Gln Gln	
152	275 280 285	

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153
154   TGC GAT GCC CAG CCA GGG GCC AGC GGG TAT GGG GTA TAT GTG AGG ATG      1076
155   Cys Asp Ala Gln Pro Gly Ala Ser Gly Tyr Gly Val Tyr Val Arg Met
156   290                      295                      300                      305
157
158   TGG AAG AGA CAG CAG CAG AAG TGG GAG CGA AAA ATT ATT GGC ATT TTT      1124
159   Trp Lys Arg Gln Gln Gln Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe
160                      310                      315                      320
161
162   TCA GGG CAC CAG TGG GTG GAC ATG AAT GGT TCC CCA CAG GAT TTC AAC      1172
163   Ser Gly His Gln Trp Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn
164                      325                      330                      335
165
166   GTG GCT GTC AGA ATC ACT CCT CTC AAA TAT GCC CAG ATC TGC TAT TGG      1220
167   Val Ala Val Arg Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp
168                      340                      345                      350
169
170   ATT AAA GGA AAC TAC CTG GAT TGT AGG GAG GGT GAC ACA GTG TTC CTT      1268
171   Ile Lys Gly Asn Tyr Leu Asp Cys Arg Glu Gly Asp Thr Val Phe Leu
172                      355                      360                      365
173
174   CCT GGC AGC AAT TAAGGTCTTC ATGTTCTTAT TTTAGGAGAG GCCAAATTGT TTTTT      1325
175   Pro Gly Ser Asn
176   370
177
178   GTCATTGGCG TGCACACGTG TGTGTGTGTG TGTGTGTGTG TGTAAGGTGT CTTATAATCT      1385
179   TTTACCTATT TCTTACAATT GCAAGATGAC TGGCTTTACT ATTTGAAAAC TGGTTTGTGT      1445
180   ATCATATCAT ATATCATTTA AGCAGTTTGA AGGCATACTT TTGCATAGAA ATAAAAAAAAA      1505
181   TACTGATTTG GGGCAATGAG GAATATTTGA CAATTAAGTT AATCTTCACG TTTTTCGAAA      1565
182   CTTTGATTTT TATTTTCATCT GAACTTGTTT CAAAGATTTA TATTAAATAT TTGGCATACA      1625
183   AGAGATATG                                     1634
184

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

- (A) NAME/KEY: Signal Sequence
- (B) LOCATION: 1...19
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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203   Met Ala Gly Ile Pro Gly Leu Leu Phe Leu Leu Phe Phe Leu Leu Cys
204                      -15                      -10                      -5
205   Ala Val Gly Gln Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro Thr Trp

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206          1          5          10
207  Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr Leu Asn Leu
208      15          20          25
209  Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu Val Ser Ser Ser
210      30          35          40          45
211  Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu Pro Thr Tyr Lys Glu
212          50          55          60
213  Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu Tyr Ala Asn Gly Ser Arg
214          65          70          75
215  Thr Glu Xaa Gln Val Gly Ile Tyr Ile Leu Ser Ser Ser Gly Asp Gly
216      80          85          90
217  Ala Xaa Xaa Arg Asp Ser Gly Ser Ser Gly Lys Ser Arg Arg Lys Arg
218      95          100          105
219  Gln Ile Tyr Gly Tyr Asp Ser Arg Phe Ser Ile Phe Gly Lys Asp Phe
220     110          115          120          125
221  Leu Leu Asn Tyr Pro Phe Ser Thr Ser Val Lys Leu Ser Thr Gly Cys
222          130          135          140
223  Thr Gly Thr Leu Val Ala Glu Xaa His Val Leu Thr Ala Ala His Cys
224          145          150          155
225  Ile His Asp Gly Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val
226          160          165          170
227
228
229  Gly Phe Leu Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp
230     175          180          185
231  Ser Thr Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val
232     190          195          200          205
233  Lys Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp
234          210          215          220
235  Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro His
236          225          230          235
237  Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys Gln Leu
238          240          245          250
239  Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp Arg Pro Gly
240          255          260          265
241  Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu Thr Tyr Asp Leu
242     270          275          280          285
243  Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala Ser Gly Tyr Gly Val
244          290          295          300
245  Tyr Val Arg Met Trp Lys Arg Gln Gln Gln Lys Trp Glu Arg Lys Ile
246          305          310          315
247  Ile Gly Ile Phe Ser Gly His Gln Trp Val Asp Met Asn Gly Ser Pro
248          320          325          330
249  Gln Asp Phe Asn Val Ala Val Arg Ile Thr Pro Leu Lys Tyr Ala Gln
250          335          340          345
251  Ile Cys Tyr Trp Ile Lys Gly Asn Tyr Leu Asp Cys Arg Glu Gly Asp
252     350          355          360          365
253  Thr Val Phe Leu Pro Gly Ser Asn
254          370
255

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/658,677

DATE: 03/27/2003
TIME: 15:31:04

INPUT SET: S36987.raw

Line

Error

Original Text